

A

SKD3 EEHPLV-FLFLGSSGIGKTELAKQTAKYMHKDAKGFIRLDMSEFQERHEVAKFIGSPPGYIGHEEGGQ--LIKKLKQCPNAVILFDEVKADHPDVLTIMLQLFDEGR
 HSP-101 PQQPTGSFLFLGPTGVGKTELAKALAEQLF--DNENQLVRIDMSEYMEQHSVSRLIGAPPGYVGHHEGGQ--LTEAVRRRPYSVVLFDEVEKAHTSVFNTLLQVLDDGRL
 TorsinA PKKPLTSL-HGWTGTGKNFVSKIIAENIVEGGLN-----SDYVHLFVATLHFPHASNITLYKQQLQWIRGNVSACARSIFIFDEMDKMHAGLIDAIPKFLD-----
 TorsinB PKKPLTSL-HGWAGTGKNFVSQIVAENLHPKGLK-----SNFVHLFVSTLHFPHQKIKLYQDQLQWIRGNVSACANSVFIFDEMDKLPKGIIDAIPKFLD-----
 TorpCel PRKPLVLSF-HGYTSGSKNYVAEIIANNIFRLGLR-----STFVQHI VATNDFPDKNKLEEQYVELRNRIILTTVQKQCRSIFIFDEADKLPEQLLGAIPKFLD-----
 Torp1 PSKPLVLSL-HGWTGTGKSYVSSLLAQHLFRDGLR-----SPHVHHSPIIHFPHPSRTEQYKKELKSWVQGNLTACERSLFLFDEMDKLPKGLMEVLQPFLG-----
 Torp2 -----AAALHQTLFIFDEAEKLPGLLEVLGPHLER-----

B

SN

SKD3 TDGKGKTIIDCKDAIFIMTSNVASDEIAQHALQLRQEALEMSRNI AENLGDVQMSDKITISKNFKENVIRPILKAHFRRDEFLGRINEIVYFLPFCHSEL IQLVNKEL
 HSP-101 TDGQGRTVDFRNTVIIMTSNLGAEHLLS-GLSGKC-TMQVARDR-----VMQEVRRQ--FRPELLNRLDEIVWFDPPLSHDQLRKVARLQM
 TorsinA YYDLVDGVSYQKAMFIFLSNAGAERTIDVALDFW-----RSGKQREDIKLDIEHALSVSVFNKK--NSGFVHSSLIDRNLIDYFVPELPLEYKHLKMCIRVEM
 TorsinB YVEQVDGVSXXKAFIFLSNAGGDLITKTALDFW-----RAGRKREDIQLKDLPEVLSVGVFNNK--HSGLWHSGLIDKNLIDYFIPFLPLEYRHVKMCMVRAEM
 TorpCel YYSTISGVDFRRSIFILLSNKGGGEIARITKEQY-----ESGYPREQLRLEAFERELMNF SYNEK-----GGGLQMSSELISNHLIDHFVPFLPLQREHVRSCVGAYL
 Torp1 PSWVVYGTNYRKAIFIFISNAGGEQINQVALEAW-----RTNRDREEISLQVEPEPVSRAVMDNP--QHGFWRSGIMEEHLLDVAVPFLPLQRHHVRHCVLNEL
 Torp2 RAPEXXGLSLXWTIFLFLSNLRGDIINEVVLKLL-----KAGWSREEITMEHLEPHLQAEIVDDH--RQWLWHSRLVKENLIDYFIPFLPLEYRHVRLCARDAF

IV

FIG. 4C

FIG. 5B

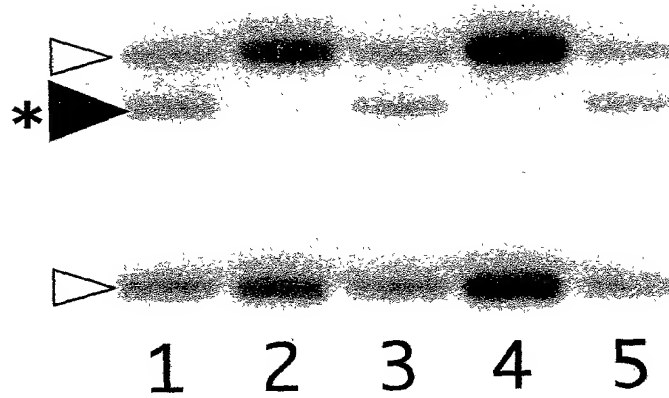


FIG. 5C

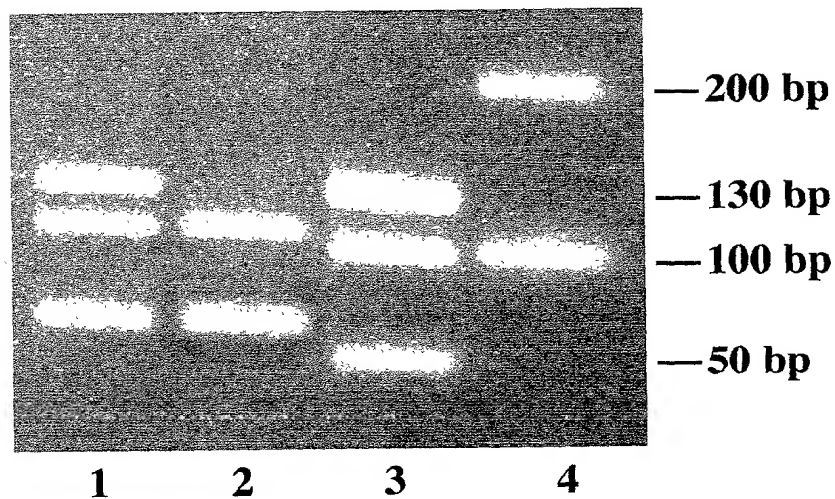
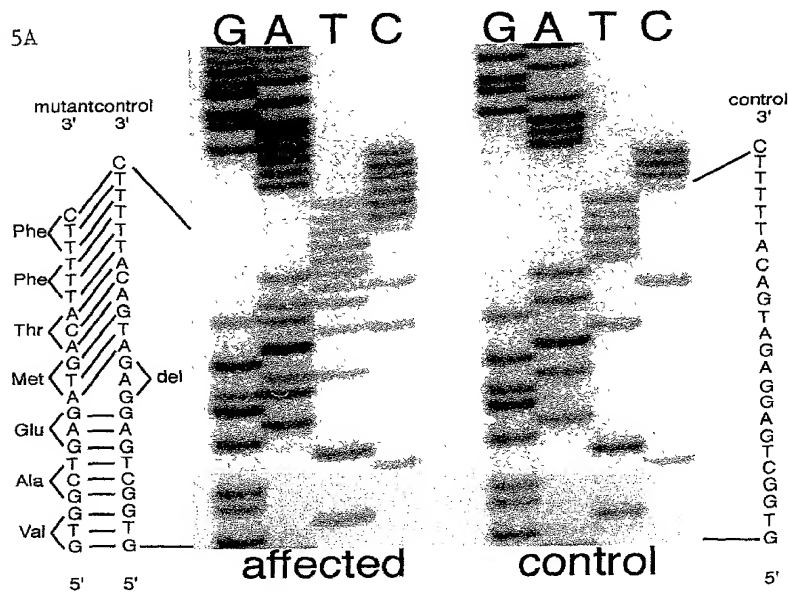


FIG. 5A



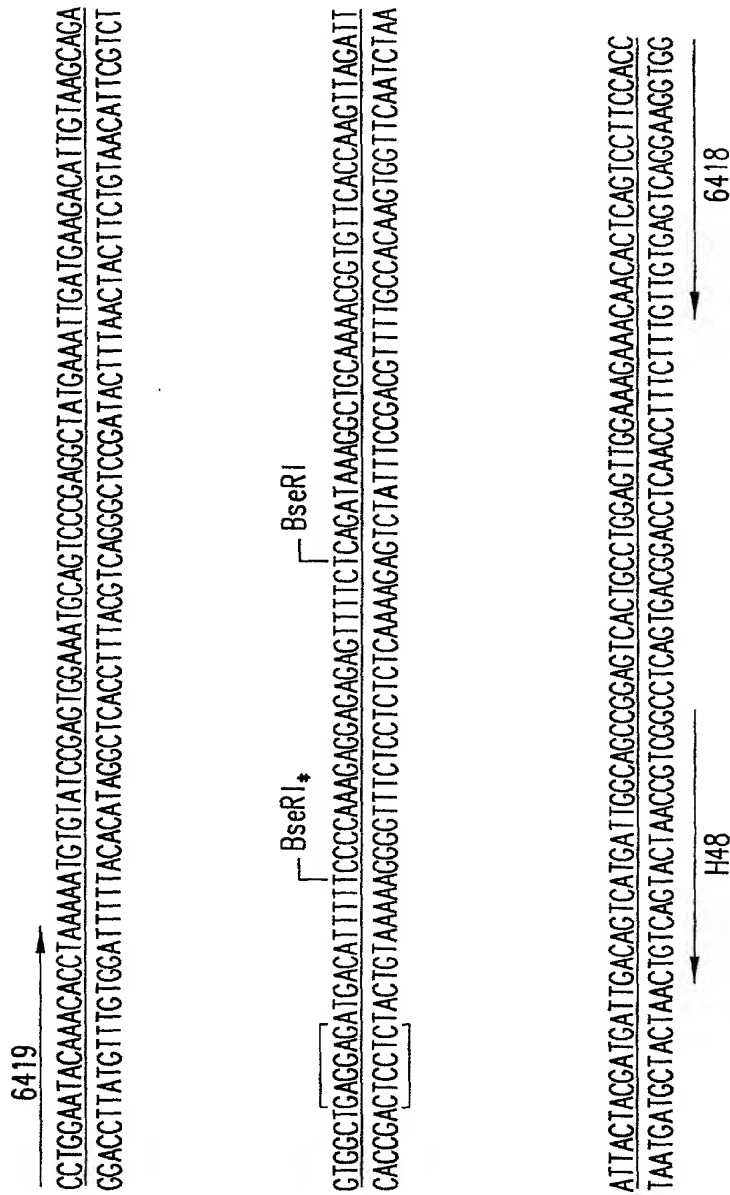


FIG. 5D

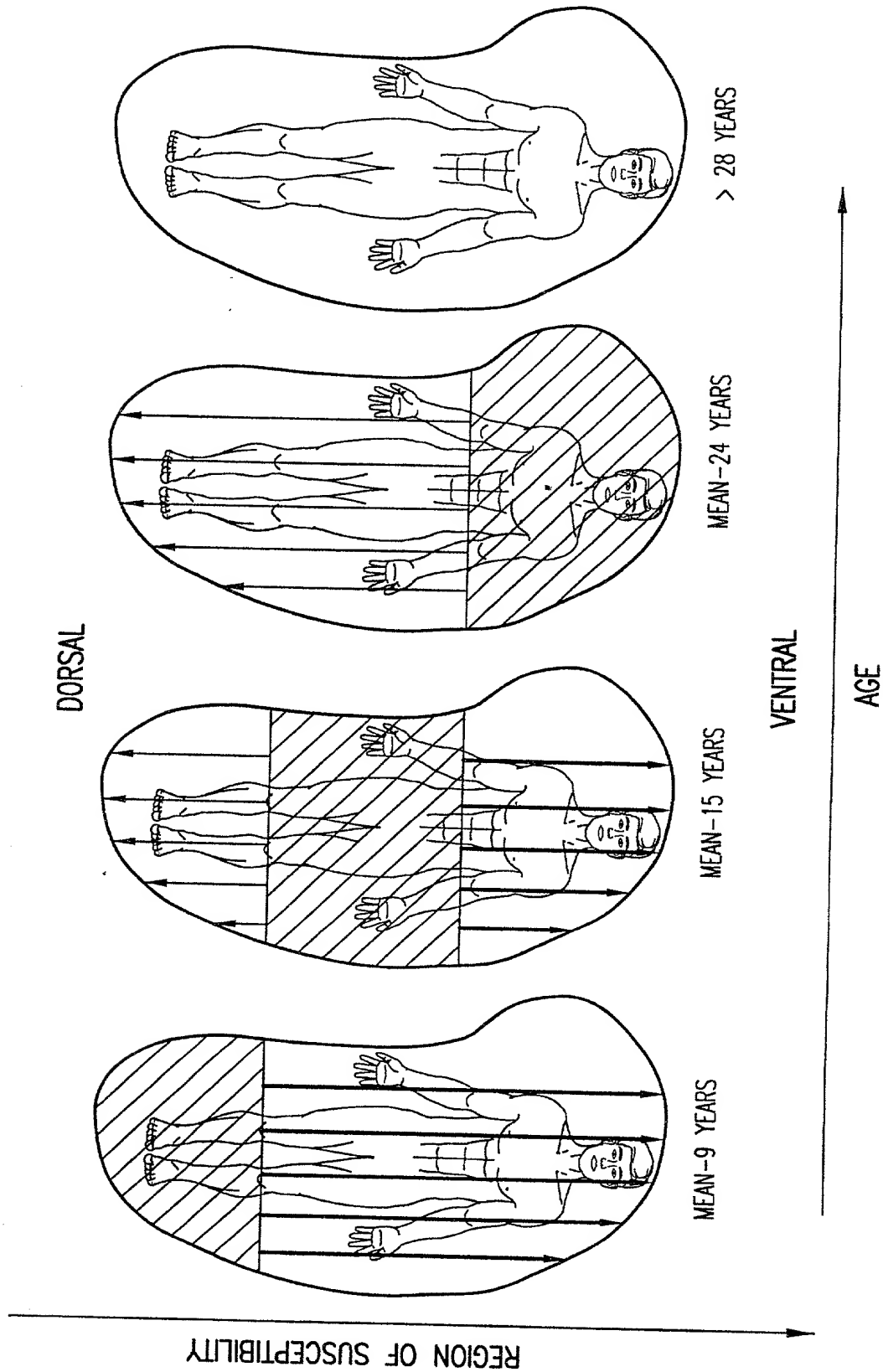


FIG.6

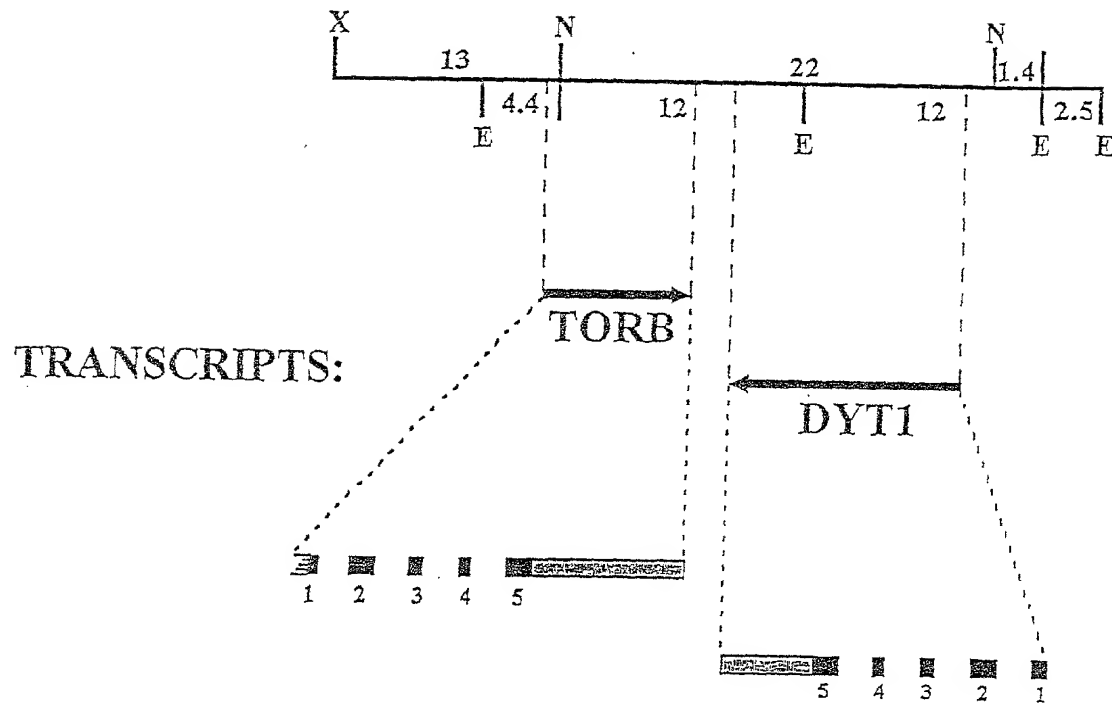


FIG. 7

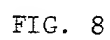


FIG. 9A

DYT1

Exon	Size (bp)	3' end of exon	5' splice site (SEQ ID NO)	Intron (kb) ^a	3' splice site (SEQ ID NO)	5' end of exon (SEQ ID NO)	Exon
1	178	...CGG GAG G R E A	GTAGGCTGGG... (67)	1.2	...TCTTTCCCAG (71)	CA CTG CAG AAG... (75) L G K	2
2	266	...TTG TAC AAG L Y K	GCAAGGATGG... (68)	1.5	...TTTAATTCAG (72)	GAT CAG TTA... D Q L	3
3	176	...TTT CTC AG F L S	GTAAGGTCAG... (69)	0.097	...TGTTTTCAG (73)	CAAT GCT GGA... (76) N A G	4
4	128	...AAG AAC AG K N S	GTGAGTAGGG... (70)	4	...TTCTTCCCAG (74)	T GGC TTC TGG... (77) G F W	5
5	251	...GAT GAT TGA D D *					

FIG. 9B

TORB

Exon	Size (bp)	3' end of exon	5' splice site (SEQ ID NO)	Intron (kb) ^a	3' splice site (SEQ ID NO)	5' end of exon (SEQ ID NO)	Exon
1	n.d.	...GCT TCG G A S A		n.d.	...GTTCTTGCAG (81)	CT CTC AAG CTG... (85) L K L	2
2	266	...CTG TAC CAG L Y Q	GCAAGAGAAC... (78)	3	...GTTGTGCCAG (82)	GAC CAG TTA... D Q L	3
3	176	...TTT CTC AG F L S	GTCAGCGGGA... (79)	1.8	...GCAAACTCAG (83)	CAAT GCA GGC... (86) N A G	4
4	128	...AAA CAC AG K H S	GTGAGTCCAC... (80)	.31	...TGTTCTGCAG (84)	T GGC CTG TGG... (87) G L W	5
5	242	...TTC CAC TGA F H *					

*Sizes of introns were approximated by gel resolution of PCR products

FIG. 10

FIG. 10 "continued"

Type	Number of Individuals	Age of onset yrs	Site of onset ^a (no.)	Sites involved (no.)
Early onset:				
AJ	5	6, 8, 8, 10, 19	A(4), ANL(1)	A(7), N(3), T(1), L(2)
NJ	12	3, 6(2), 8, 9, 10, 11, 13, 14(2), 16, 18	A(9), AU(1)	A(20), G(9),
			G(1), L(1)	R(6), K(4), U(4), L(4),
				N(6), P(1), S(1), T(2),
				F(2), J(3), U(2)
Potential homozygosity:				
AJ ^b	5	4, 6, 7, 26, 35	L(4), M(1)	L(4), M(1), N(2), P(1),
				T(1), U(1), H(2)
Late onset:				
AJ	1	66	U	U

^a Body sites: U=upper face, F=lower face, J=jaw, T=tongue, P=pharynx, L=larynx, S=speech, swallowing, A=arm, K=trunk, G=leg, N=neck, H=hearing loss.
(no.=Number of individuals in group with that site affected.)

^b Three of these individuals had all known AJ ancestors, one was 7/8 AJ, and one was 1/2 AJ.

Sample number	Genotype			
	D9S2160 ^a	D9S2161	D9S63	D9S2162
18843	3,4	2,2	8,8	4,4
13709	4,4	2,6	14,14	NT ^b
14122 ^c	3,3	4,4	0,0	5,5
13945	4,4	1,5	18,18	NT ^b
14040	2,5	1,2	16,16	2,4

^a Markers listed from centromere to telomere: D9S2160 - <40 kb - D9S2161 - 150 kb - D9S63 - 130 kb - D9S2162 (Ozelius *et al.*, 1997a).

^{*} Position of DYT1 gene

^b Not tested.

^c This individual had onset at 7 years in the arm with eventual involvement of the arm and neck and a positive family history of movement disorder (father with tremor). He was also apparently homozygous for markers D9S159-D9S2158-D9S2159, which are proximal to DS2160 (total region of 100 kb).

FIG. 11

FIG. 12A

Intron Primers Used to Amplify DYT1 Exons			
Exon	Primer Sequence (5' → 3')	SEQ. ID NO.:	Product Size (bp)*
1	GCAAAACAGGGCTTTGTACCG	(SEQ. ID NO.: 30)	
	AGTAGAGACGCGGGTAGATG	(SEQ. ID NO.: 31)	
	GCGTCTCTACTGCCTCTTCG	(SEQ. ID NO.: 32)	
	ATGCCCTGGTCCTAGTTCAG	(SEQ. ID NO.: 33)	
2	GGTTTCGCAAGGTGCTTGGA	(SEQ. ID NO.: 34)	408
	GGGATTCCAACTTCCATCC	(SEQ. ID NO.: 35)	
3 and 4	TCCATGGGGTTGGTAGGAAC	(SEQ. ID NO.: 36)	804
	GGTGACAGAGTAAACTATCTG	(SEQ. ID NO.: 37)	
5	GACCCCCAGTAGACGTTTGT	(SEQ. ID NO.: 38)	640
	GTAAAAAATCATGAGCCCTGC	(SEQ. ID NO.: 39)	

FIG. 12B

Intron Primers Used to Amplify TORB Exons			
Exon	Primer Sequence (5' → 3')	SEQ. ID NO.:	Product Size (bp)*
1	n.d. [#]		-
2	CCAGAGTTAGTGAGCAGGTC	(SEQ. ID NO.: 40)	526
	GAAGCGTTAAGGACCTCCAC	(SEQ. ID NO.: 41)	
3	ATCTATCTCTGCCAATTCCAC	(SEQ. ID NO.: 42)	466
	GTCCTGGTAAACAAAGTGCTG	(SEQ. ID NO.: 43)	
4	TGGGGTTACTCTATGTTGGTC	(SEQ. ID NO.: 44)	440
	CTAGCACAGTATGCCCTAAG	(SEQ. ID NO.: 45)	
5	TGAGGAATGTGCTGAGGGTC	(SEQ. ID NO.: 46)	333
	GCTGTCTCCTACCCCATCTG	(SEQ. ID NO.: 47)	

*PCR products were generated using oligonucleotides synthesized from intronic sequences, and accordingly the size of each product includes both intron and exon sequence.

[#]Not done. It was not possible to identify primers which could consistently PCR this exon.

<i>Protein</i>	<i>Organism</i>	<i>Gene</i>	<i>Locus</i>	<i>Accession</i>	<i>UniGene</i>
hTorsinA	human	DYT1	Chr.9, D9S159-D9S164	AF007871	Hs.19261
mTorsinA	mouse			AA230756	Mm.40438
rTorsinA	rat			AA850233	Rn.20041
sTorsinA	pig			AU058534	
hTorsinB	human	TORB	Chr.9, D9S159-D9S164	AF007872	Hs.5091
mTorsinB	mouse			AA596988	
drTorsinC	zebrafish			AA542632	
hTorp1	human	TORP1		AA873275	Hs.59038
mTorp1	mouse			AA981789	Mm.33875
rTorp1	rat			H31561	
hTorp2	human	TORP2		AA150869	Hs.26267
mTorp2	mouse			AA791729	
dmTorp3	fruitfly	EG:84H4.1	DMC84H4	AL031766	
ceTorp4A	nematode	F44G4.1	CEC18E9	P54073	
ceTorp4B	nematode	Y37A1B.12	CEY37A1B	AL023835	
ceTorp4C	nematode	Y37A1B.13	CEY37A1B	AL023835	

FIG. 13

INTRON 1 OF DYT1 GENE

FIG. 14A: Clone 1:

23g14-2-7050.cDNA (Length: 283) SEQ ID NO.: 48

```

1   gtaggctggg gcgggggctg gaggctgggg ctggggctgg ggctgggcga
51  tggcactagg gctgaactag gaccagggca tggagaatgg aggatggagg
101 cggggggatg gcaccagggc cgggctagga ctagggctgg agcggggcct
151 gggggctggg gctgggcgat ggcactaggg cgggttgggg ctggggctgg
201 ggctggggga tggagcgggg cggggggctg ggggtggggc tgggggatcg
251 actagggctg gnttaggacc aggcgggttg cat
  
```

Bold = primer 4 (reverse sequence) from FIG. 12A

Underline = 5' splice sequence from Intron 1 FIG. 9A

FIG. 14B: Clone 2:

Harvey7-23g14-2.cDNA (Length: 375) SEQ ID NO.: 49

```

1   ggatggtgga tggaggctgg gggatggcag tagggccggg ctaggactgg
51  ggctggagcg gagtttgggg ctggggctca ggagcggggg ctggggctgg
101 ggctggggct ggggggatggc actagggcag gccggggtag gggtcacatc
151 ccaggagggc cgggctgggc agagctgagt ccgcgggggc cggaccccg
201 aagccaagcn gccggcctgc aggatgaggc ctggctcctc ggccatgacc
251 acagacgtgc cagacttaag tacggagacc tgaggagcca ggctgcagtt
301 ggcctacttt ncnctaagct gggggtggac cagtggtaac ctccctcgaa
351 gtgggttctg ctctttctag cctag
  
```

FIG. 14C: Clone 3:

23g1-Harvey11.cDNA (Length: 439) SEQ ID NO.: 50

```

1   ccactgccac tgccaccagt ttgcaacctt aacctctgtc ctgctcctcc
51  ccccccaagg cagagccggn gaaaggaaac agtttggtcc ctccctggtc
101 gctgcggaag agtctcacca tccttctgtc tccgtagcta gaaaggaggc
151 agaaccacac ttcggaggga ggttaccact ggtccacccc cagcttagcg
201 caaagtaggc caacctgcat gcctggnnct cctcaggntc tgctactta
251 agtctggcag ctctnnntca tggccgaggt agccaggctc atcctgcagg
301 nncnngcenn ttgncttncc ggggtntcgn nccccgtac tcagctcgtc
351 cagccggcct ctggatgtga cctaccgctg ctagtgcac ccagccagcc
401 agccagccgt ctagccagcc aactgctcag ccagtctag
  
```

FIG. 14D: Clone 4:

23g1-Harvey6.cDNA (Length: 378) SEQ ID NO.: 51

```

1   ctgggaaaga caaagccaat caggagtggg gaagaaacac ggcaaaatgt
51  agccacattt acagcccata aganagccag caaagccgtc tagcctccaa
101 gcaccttgcg aaacctcaag tactgcggtc tggtaagctc ctggcccaga
151 ggggacggcg gtccaggng cctccctttt gctggtcctg cctattctaa
201 agccctggcc cgnctccttc cggaaaagcc ccttggtgcc actgccactg
251 ccaccanttt gcnnccctac ccctgtntctg ctcctccac cccaaggcag
301 atgcggnnng ngaaaggaaa cantttggtc cctcctggtc ggctcgnnga
351 agactcctca ccatccttcc tgtcttcc
  
```

Bold = primer 5 from FIG. 12A

Italics = sequence overlap between Clone 4 and Clone 3

Underline = 3' splice site from FIG. 9A

[illegible]

INTRON 2 DYT1 GENE

FIG. 15A: Clone 1:
29a5-6343.cDNA (Length: 400) SEQ ID NO.: 52

```
1    gaatattttac gaggggtgggc tgaacagtga ctatgtccac ctgtttgtgg
51   ccacattgct ctttccacat gcttcaaaca tcaccttgta caaggcaagg
101  atggaagttt ggaatccctt cctggatgtc atcgggtttg gggctctctt
151  gttgtgggat gagatttggg agttctatgt tgaaatgagt gagccccgaa
201  aacggttcat gtctcagttc cccttggaaa ggtgtagaag ttaagagttt
251  gagatgcgtg gagcagttaa taccatcaaa gctttgtggg gggttctgaa
301  aatcgggtcca gtgagtatgt agggtcattg gatttttagag gtggacatga
351  tcaaatccat cttagagatc aacacatctc actcattttt attttcttat
```

Bold = primer 6 from FIG. 12A
Underline = 5' splice site sequence for intron 2 from FIG. 9A

FIG. 15B: Clone 1:
29a5-6343.cDNA (Length: 402) SEQ ID NO.: 89

```
1    gaatattttac gaggggtgggc tgaacagtga ctatgtccac ctgtttgtgg
51   ccacattgct ctttccacat gcttcaaaca tcaccttgta caaggcaagg
101  atggaagttt ggaatccctt cctggatgtc atcgggtttg gggctctctt
151  gttgtgggat gagatttggg agttctatgt tgaaatgagt gagccccgaa
201  aacggttcat gtctcagttc cccttggaaa ggtgtagaag ttaagagttt
251  gagatgcgtg gagcagttaa taccatcaaa gctttgtggg gggttctgaa
301  aatcgggtcca gtgagtatgt agggtcattg gatttttagag gtggacatga
351  tcaaatccat cttagagatc aacacatctc actcattttt attttcttat
401  tt
```

Bold = primer 6 from FIG. 12A
Underline = 5' splice site sequence for intron 2 from FIG. 9A

FIG. 15C: Clone 2:
6550-54a5s.cDNA (Length: 418) SEQ ID NO.: 53

```
1    tttggagtgac gacaggactg ggttcagggt ccagctctgc cacatatagt
51   cttgggcaag tggagtaagc gctctctgtg cctcagttcc ctcattctgta
101  aaatgagaac gatagtggcc actccatggg gttggttagga acaaagaaga
151  ttttgggcat gttaaagttct tagtgccgag tgcacagtgg tctgtaagtg
201  aagctgcggt tcttagtggt agaaggagct gattgatggc cctgggtgag
251  aacttttgtgt tcgctttttc ccnttttaat tcaggatcag ttacagttgt
301  ggattcgagg caacgtgagt gcctgtgcga ggtccatctt catattttgat
351  gaaatggata agatgcatgc aggcctcata gatgccntca anccttttct
401  cgactattat gacctggt
```

Bold = primer 7 from FIG. 12a
Underline = 3' splice sequence for intron 2 from FIG. 9A
Italics = EXON 3 sequence

INTRON 3 DYT1

FIG. 16A: Clone 1:

6202-54a5.cDNA (Length: 198) SEQ ID NO.: 54

```
1      ctcgactatt atgacctggt ggatgggggtc tcctaccaga aagccatggt
51     catattttctc aggtaagggtc agggctagga catgatggat gggccccgag
101    cccaagcctc tgagctccag gagaaaaccc tgccttacc cactgggatt
151    gttttgcagc aatgctggag cagaaaggat cacagatgtg tttggatt
```

FIG. 16B: Clone 1:

6202-54a5.cDNA (Length: 200) SEQ ID NO.: 90

```
1      ctcgactatt atgacctggt ggatgggggtc tcctaccaga aagccatggt
51     catattttctc aggtaagggtc agggctagga catgatggat gggccccgag
101    cccaagcctc tgagctccag gagaaaaccc tgccttacc cactgggatt
151    gttttgcagc aatgctggag cagaaaggat cacagatgtg gctttggatt
```

Bold = EXON

Underline = sequence from for 5' splice site sequence and 3' splice site sequence, respectively from FIG. 9A

6202-54a5.cDNA (Length: 200) SEQ ID NO.: 90

INTRON 4 DYT1

FIG. 17A: Clone 1:

Intron 4-5 prime.cDNA (Length: 535) SEQ ID NO.: 55

1 GTCTGTGTCG GTTTTCAATA ACAAGAACAG GTGAGTAGGG CCATCCACCG
51 CCAGTCCCAT CTGGTTCCTA ATCCTGCACC CTAAGTGTTA AAAGCATCAG
101 GGTCACGTGC AGCATCACCT GGGAGCTGGG TAGAAAGAAA TGgAGATTCT
151 CAGTCCCCTT CCGAGTCATG AGGGGAATCT TTGCTGATGA ACTCCAGGTA
201 ACTTTTATGA AACTAATGT TTGACAAGTG CTGTTTTATT TTTATTTTTC
251 **AGATAGTTTT** **ACTCTGTCAC** CTAGGCTGGA GTGCAGTGGC GTAACCTTGC
301 CTCACGTCAA CCTCTGCCTC CCGGGCTCAA GCGATTCTTG TGCCTCAGCC
351 TCCTGAGTAG CTGGGATTAC AGGTGCACAC CATGCCCAAG CNAATATTTT
401 GTATTTTTAG TAGAGANGGG GCCCCGTNCA TGTAAACCAG GCTGGTCTTG
451 AACTNTTACC TCAGGTGAGT CCNCCACCTC GGCCTCCCAA AGTGCTGGGA
501 TTACAGGCGT GAGCCACTGT GTCTCAGCTT ATTTTT

Italics = EXON sequence

Underline = 5' splice sequence from FIG. 9A

Bold = primer 8 from FIG. 12A

FIG. 17B: Clone 2:

Intron 4-3 prime.cDNA (Length: 1302) SEQ ID NO.: 56

1 GCCACTCCAA GCTACCATCT GAGATTGTTT CCTGCCCTAG AGTGGTAAAG
51 GCGTGAGGTC CGTCTGCCCT CAGCTGTGTC CCCAGGCCCA GGGCGTGCCT
101 GGCAACANNA GCAGGCCTCT GAGAACCAGC CTCCCACGTG AGTTCATGAT
151 AGNAAGACAG CCCCTCGTTC CCATTCACTG GTTGTTCTG TTCTTTYCCT
201 GGCMATAAGC TCCACTCTGY MRTCAGCCAM ACATTTATTG AGTACCAGTT
251 GTTGCCAAAG CACTGTTGGG CATGAAAAGC ATTAACCCAG TGAATGAGGA
301 GGAGCTTGGG TTGGGACGGA GCCMCARAAW TACATGGCAG ACCAGAAGGA
351 AATCAGCTCA AGTAGAAARA CACGCATGGG CTCGTGGGCG ACGCAGTGTG
401 TGCTGTGTCA TCTGGGGCTG GGAGGAAGTG TCCTGGATCA GGAGTTCCAG
451 GAGCCCAGGA GGAGTGGACG GGTCAGTGCA GAGCCAGCCC GCAATCAGGG
501 GAAGAAAACA CGGCCAAGGC CAGGCCTTCA CGGGGAGCCC AGCGTGGGCT
551 GCACATCTGC ACTCTCCAGG CTAGTTTTGG TGCCCACATG CTCTGCAGGG
601 TCTGGGCACT GTGGCAGCGG CAGCAGGCTT CCCTGTTGCT AGTCCAGCTG
651 CTGAAACTCC AGGGAGAGTC AAAAAGTTCC CAAATACAGA GGCGTGGCTG
701 GTAGTCCTTC CCGGGAATTC TTCTTGCTTC CCGCTTTCTG TGGAACCTCTG
751 CCTTCCCCAC TCTGCCTCTC TGCTTGTTCC TGGGCCCCAG GACCTCTTTC
801 CCATCTTCGA TCTCTTAAGT CATACTTGG GAGGCCTCCC CCAGCCCGCC
851 GTGTAAAGAG GGCTGTCACA GCTTCTGCTG TCACAGAAGC ATTACAATGT
901 GCAGGTGCCT GTTAACATCT GCCTTCCCCA CTGATCTGGA GCTCCACAAG
951 GGAGAGGGCA CACCCAGTAG GTATGTGTGG GATGGATAGG AGGGTGGATG
1001 ACACCCAGTA GATGTGTATG GGATGGATAG GAGGGTGGAT GACACCCAGT
1051 AGGTGTGTAT GGGATGGATG GGAGGGTGGG TGACCCCTAG TAGATGTGGG
1101 GGGGGTGGGT GGGTGACCCC CAGTAGGTGT GTGTGGCATG GATAGGT**GAC**
1151 **CCCCAGTAGA** **CGTTTTGTGGG** ACGGATGGGA GGGTAGGTAA GTGACCCCCA
1201 GGAGGCGTCT ATAGGGCAGG TGGGTGGATG TGGATGAACA GCACCTTGTT
1251 TCTTCTTCCC AGGTGGCTTC TGGCACAGCA GCTTAATTGA CCGGAACCTC
1301 AT

Bold = primer 9 in FIG. 12A

Underline is 3' splice site sequence from FIG. 9A

Italics is EXON 5 sequence

INTRON 1 5' from TORB

FIG 18A: Clone 1:
h59-29a5.se (Length: 240) SEQ ID NO.: 57

```
1      ggagcgggccg ctcaacgctt cgggtacggc gcgcgcgcga gctgtgggtc
51     ggcgctgcgg ggggcgcggg ggcgcggggg cgcggaggga cggcctcgtg
101    ggcgcctggc acggaccggg cccgtggcat ctagacggcg gtgggtcccag
151    ctgggggtggg cggggagcgg atggggcggc cccggaaccg ttcgcnggaa
201    cgcagaagcn gtgccttgaa acactctcag atcgtgnggc
```

INTRON 1 3' from TORB

FIG. 18B: Clone 2:
5667s-29a5.Se (Length: 310) SEQ ID NO.: 58

```
1      gggaccaaag gacgtccgtc gttcccaccg accctaateg ttcgcgngtc
51     ngttcgctac ccagtagaga gacttactta cnngtnnatc gaaggaatag
101    tctggggcctt cgcaattcct ggagggtgtat tagaactttc accgtagcaa
151    actgacggag ccgggatccc acaccgcctg tgggnncgac acgggaccta
201    ttgacacgaa gaacgaaacn gtcgattctt tcacgacgca acgactacgt
251    aaaaattcca gacaaagaga gaaacaagac cccgacaaga acgtcGAGAG
301    TTCGACCTAA
```

Upper Case Letters = EXON (bottom strand)
Underline = sequence from Table 1
Bold = 2nd primer from FIG. 12B

INTRON 2 5' from TORB

FIG. 19A: Clone 1:
6101-29a5.Se (Length: 401) SEQ ID NO.: 59

1 CAGGAACAAC AAAAATCCCA AGAAACCACT GACCCTTTCC TTACACGGCT
51 GGGCTGGCAC AGGCAAGAAT TTTGTCAGTN AAATTGTGGC TGAAAATCTT
101 CACCCAAAAG GTCTGAAGAG TAACTTTGTC CACCTGTTTG TATCGACTCT
151 GCACTTCCCT CATGAGCAGA AGATAAAACT GTACCAGgca agagaacccg
201 ctattatctc gtctgcaggc cagtcggact ggtccgggtg **acctgctcac**
251 **taactctggc** ctctgcttct ctttcctttg tggttgcgtgta gcccccggt
301 ccactgagtt aaggcacact tagtccaggt agttacaaag ctctcctaca
351 acattttctta cttgggttcca aaacagtcca gtggggtagg ggatgttatt
401 t

Upper Case Letters = EXON
Underline = 5'splice site sequence from FIG. 9B
Bold = 1st primer from FIG. 12B

INTRON 2 3' TORB

FIG. 19B: Clone 2:
29A5-39-11.se (Length: 238) SEQ ID NO.: 60

1 ttctgtaact ggtcCTGGAC CAACCATGAA AGAAGAAACA GGATGCGAAG
51 CTCAAAGGGC TGCACCAAGA GGCGCGCAGG CTCCATCTGC TCCTCATGCA
101 CTGAAGGACG AGGTCAGAGC TCTTAGAATG GCACCCTCAC CCCCACTCGC
151 TAGGTAGCAG CTTTTCTAAA ACCTTATCTC TAAAAAGTGG **AAATTGGCAG**
201 **AGATAGATGC** TAAATGCAG AGAAGTTTTT CCTAACTC

Lower Case Letters = EXON
Underline = sequence from Table 1
Bold = primer 3 from FIG. 12B

FIG. 19A-19B

INTRON 3 5' TORB

FIG. 20A: Clone 1:

39-14-29a5.Se (Length: 391) SEQ ID NO.: 61

```
1      GGGATCATTG ACGCAATCAA GCCGTTTCTA GACTACTACG AGCAGGTTGA
51     CGGAGTGTCT TACCGCAAAG CCATCTTCAT CTTTCTCAGg tcagcgggag
101    gcggtttttt ggggcacaca agcccttcat tctctcaatg ataaaatgag
151    gtcctgagga ccatcagcac tttgtttacc aggacgaaag tgccctgcttg
201    gcacaaggca cttacctact gctttacttt tcctttgccg gtcctcagca
251    tggcacacag tgtgggttgt ggaaatgaac taaagaaata atcactggga
301    caggcgcggt ggctcacacc tgtcaatccn agcactttgg gnaggcatgg
351    cgggcgggatc acaggagatc gagacatctg ctaacatgnt g
```

Upper Case Letters = EXON

Underline = 5' splice site sequence from FIG. 9B

Bold = primer 4 from FIG. 12B

INTRON 3 3' TORB

FIG. 20B: Clone 2:

5665s-54a5.Se (Length: 373) SEQ ID NO.: 62

```
1      gtaagacaca gagtcttttt tnttttttag accgagtntc attnttggtg
51     ccnangctgg agtgcaatgg catgatctcg gctcgctgca acctccacct
101    cccggrttca aacgattctc ccacctcagc ctcccatgta gctgggatta
151    cagncatgca ccaccattag cctggctaata ttttggtgtt ttagtagaga
201    tggtgttact ctatgttggg caggctggcc ttgaactccc gacctcaggt
251    gatctacctg cctcggcctc ccaaagtgtc gggattacag ccatgagcna
301    ccacnscnan cagacncaga agtccttaata tgtgatttta atctttattt
351    ctctggcaaaa ctcagCAATG CAG
```

Upper Case Letters = EXON

Underline = 3' splice site sequence from FIG. 9B

Bold = primer 5 from FIG. 12B

INTRON 4 TORB

FIG. 21: Clone 1:
intron4torb.se (Length: 310) SEQ ID NO.: 63

```
1      gtgagtccac cagggtaaag gagcccotta actgtccagc agtgagccgt
51     ctgctctttc attgagtgtt tgcacaaagc cacaggatcc cactggattt
101    cctcactttg ctaaagtcag gaattttctt agggcatact gtgctagaaa
151    ccagtgagtg agtgtccagc tgagtcctcg atgggcttgt tgcacactga
201    caagagacnc tctcaagggg tacggacatg aggaatgtgc tgagggtcgg
251    gactggagct tggccaggtg gcggtggtgg caggaaaccc agctgtgtct
301    tggtctgcag
```

Underline = 5' splice site sequence from FIG. 9B

Bold = primer 6 from FIG. 12B

Underline italics = 3' splice site sequence from FIG. 9B

Bold italics = primer 7 from FIG. 12B

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